

10/521518

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.**

Application Serial Number: 10/521,518
Source: PSR
Date Processed by STIC: 5/24/06

ENTERED

CRF Errors Edited by the STIC Systems Branch

Serial Number: 10/521,518

CRF Edit Date: 5/24/06
Edited by: AS

— Realigned nucleic acid/amino acid numbers/text in cases where the sequence text "wrapped" to the next line

— Corrected the SEQ ID NO. Sequence numbers edited were:

— Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited:

— Deleted: ___ invalid beginning/end-of-file text ; ___ page numbers

— Inserted mandatory headings/numeric identifiers, specifically:

— Moved responses to same line as heading/numeric identifier, specifically:

J

Other:

corrected amino acid numbering in Seqs. 19,21,25
corrected L1407, L1417 lines



PCT

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/521,518

DATE: 05/24/2006
TIME: 13:48:28

Input Set : A:\PTO.AMC.txt
Output Set: N:\CRF4\05242006\J521518.raw

3 <110> APPLICANT: Expressive Research B.V.
 5 <120> TITLE OF INVENTION: Modulating developmental pathways in plants
 7 <130> FILE REFERENCE: P59845PC00
 C--> 9 <140> CURRENT APPLICATION NUMBER: US/10/521,518
 C--> 9 <141> CURRENT FILING DATE: 2005-01-18
 9 <150> PRIOR APPLICATION NUMBER: PCT/NL03/00524
 10 <151> PRIOR FILING DATE: 2003-07-17
 12 <150> PRIOR APPLICATION NUMBER: EP 02077908.8
 13 <151> PRIOR FILING DATE: 2002-07-17
 15 <160> NUMBER OF SEQ ID NOS: 110
 17 <170> SOFTWARE: PatentIn version 3.2
 19 <210> SEQ ID NO: 1
 20 <211> LENGTH: 227
 21 <212> TYPE: PRT
 22 <213> ORGANISM: Arabidopsis thaliana
 24 <400> SEQUENCE: 1
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 27 1 5 10 15
 30 Pro Pro Pro Ala Pro Lys Gly Tyr Tyr Arg Arg Gly His Gly Arg Gly
 31 20 25 30
 34 Cys Gly Cys Cys Leu Leu Ser Leu Phe Val Lys Val Ile Ile Ser Leu
 35 35 40 45
 38 Ile Val Ile Leu Gly Val Ala Ala Leu Ile Phe Trp Leu Ile Val Arg
 39 50 55 60
 42 Pro Arg Ala Ile Lys Phe His Val Thr Asp Ala Ser Leu Thr Arg Phe
 43 65 70 75 80
 46 Asp His Thr Ser Pro Asp Asn Ile Leu Arg Tyr Asn Leu Ala Leu Thr
 47 85 90 95
 50 Val Pro Val Arg Asn Pro Asn Lys Arg Ile Gly Leu Tyr Tyr Asp Arg
 51 100 105 110
 54 Ile Glu Ala His Ala Tyr Tyr Glu Gly Lys Arg Phe Ser Thr Ile Thr
 55 115 120 125
 58 Leu Thr Pro Phe Tyr Gln Gly His Lys Asn Thr Thr Val Leu Thr Pro
 59 130 135 140
 62 Thr Phe Gln Gly Gln Asn Leu Val Ile Phe Asn Ala Gly Gln Ser Arg
 63 145 150 155 160
 66 Thr Leu Asn Ala Glu Arg Ile Ser Gly Val Tyr Asn Ile Glu Ile Lys
 67 165 170 175
 70 Phe Arg Leu Arg Val Arg Phe Lys Leu Gly Asp Leu Lys Phe Arg Arg
 71 180 185 190
 74 Ile Lys Pro Lys Val Asp Cys Asp Asp Leu Arg Leu Pro Leu Ser Thr
 75 195 200 205
 78 Ser Asn Gly Thr Thr Ser Thr Val Phe Pro Ile Lys Cys Asp

R.6

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Input Set : A:\PTO.AMC.txt
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83	225		
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87	<211> LENGTH: 416		
88	<212> TYPE: PRT		
89	<213> ORGANISM: Arabidopsis thaliana		
91	<400> SEQUENCE: 2		
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94	1 5 10 15		
97	Thr His Phe Asp Leu Glu Ser Asn Asn Asn Leu Gln Tyr Ser Leu Ser		
98	20 25 30		
101	Leu Asn Leu Ser Ile Arg Asn Ser Lys Ser Ser Ile Gly Ile His Tyr		
102	35 40 45		
105	Asp Arg Phe Glu Ala Thr Val Tyr Tyr Met Asn Gln Arg Leu Gly Ala		
106	50 55 60		
109	Val Pro Met Pro Leu Phe Tyr Leu Gly Ser Lys Asn Thr Met Leu Leu		
110	65 70 75 80		
113	Arg Ala Leu Phe Glu Gly Gln Thr Leu Val Leu Leu Lys Gly Asn Glu		
114	85 90 95		
117	Arg Lys Lys Phe Glu Asp Asp Gln Lys Thr Gly Val Tyr Arg Ile Asp		
118	100 105 110		
121	Val Lys Leu Ser Ile Asn Phe Arg Val Met Val Leu His Leu Val Thr		
122	115 120 125		
125	Trp Pro Met Lys Pro Val Val Arg Cys His Leu Lys Ile Pro Leu Ala		
126	130 135 140		
129	Leu Gly Ser Ser Asn Ser Thr Gly Gly His Lys Lys Met Leu Leu Ile		
130	145 150 155 160		
133	Gly Gln Leu Val Lys Asp Thr Ser Ala Asn Leu Arg Glu Ala Ser Glu		
134	165 170 175		
137	Thr Asp His Arg Arg Asp Val Ala Gln Ser Lys Lys Ile Ala Asp Ala		
138	180 185 190		
141	Lys Leu Ala Lys Asp Phe Glu Ala Ala Leu Lys Glu Phe Gln Lys Ala		
142	195 200 205		
145	Gln His Ile Thr Val Glu Arg Glu Thr Ser Tyr Ile Pro Phe Asp Pro		
146	210 215 220		
149	Lys Gly Ser Phe Ser Ser Glu Val Asp Ile Gly Tyr Asp Arg Ser		
150	225 230 235 240		
153	Gln Glu Gln Arg Val Leu Met Glu Ser Arg Arg Gln Glu Ile Val Leu		
154	245 250 255		
157	Leu Asp Asn Glu Ile Ser Leu Asn Glu Ala Arg Ile Glu Ala Arg Glu		
158	260 265 270		
161	Gln Gly Ile Gln Glu Val Lys His Gln Ile Ser Glu Val Met Glu Met		
162	275 280 285		
165	Phe Lys Asp Leu Ala Val Met Val Asp His Gln Gly Thr Ile Asp Asp		
166	290 295 300		
169	Ile Asp Glu Lys Ile Asp Asn Leu Arg Ser Ala Ala Ala Gln Gly Lys		
170	305 310 315 320		
173	Ser His Leu Val Lys Ala Ser Asn Thr Gln Gly Ser Asn Ser Ser Leu		

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Input Set : A:\PTO.AMC.txt

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174	325	330	335
177	Leu Phe Ser Cys Ser Leu Leu Leu Phe Phe Leu Ser Gly Asp Leu		
178	340	345	350
181	Cys Arg Cys Val Cys Val Gly Ser Glu Asn Pro Arg Leu Asn Pro Thr		
182	355	360	365
185	Arg Arg Lys Ala Trp Cys Glu Glu Asp Glu Glu Gln Arg Lys Lys		
186	370	375	380
189	Gln Gln Lys Lys Lys Thr Met Ser Glu Lys Arg Arg Arg Glu Glu Lys		
190	385	390	395
193	Lys Val Asn Lys Pro Asn Gly Phe Val Phe Cys Val Leu Gly His Lys		
194	405	410	415
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198	<211> LENGTH: 1634		
199	<212> TYPE: DNA		
200	<213> ORGANISM: Arabidopsis thaliana		
203	<220> FEATURE:		
204	<221> NAME/KEY: CDS		
205	<222> LOCATION: (501)..(563)		
206	<223> OTHER INFORMATION: signal sequence (exon 1)		
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209	<221> NAME/KEY: CDS		
210	<222> LOCATION: (655)..(708)		
211	<223> OTHER INFORMATION: propeptide (exon 2)		
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215	<222> LOCATION: (797)..(856)		
216	<223> OTHER INFORMATION: propeptide (exon 3)		
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219	<221> NAME/KEY: CDS		
220	<222> LOCATION: (955)..(1131)		
221	<223> OTHER INFORMATION: conserved cysteine motif (exon 4)		
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224	attaaacgcgc aaacactaca tctgtgtttt cgaacaatat tgcgtctgcg tttccttcat	60	
226	ctatctctc cagtgtcaca atgtctgaac taagagacag ctgtaaacta tcattaagac	120	
228	ataaaactacc aaagtatcaa gctaattgaa aaattactct catttccacg taacaaattg	180	
230	agtttagctta agatatttagt gaaaacttaggt ttgaatttgc ttcttcttct tccatgcac	240	
232	ctccgaaaaa agggaaccaa tcaaaaactgt ttgcataatca aactccaaca ctttacagca	300	
234	aatgcaatct ataatctgtg atttatccaa taaaaacctg tgatttatgt ttggctccag	360	
236	cgtatggaaatg ctatgcatgt gatctctatc caacatgagt aattgttcag aaaataaaaa	420	
238	gtatgtatata taaagaatca tccacaagta ctatcccac acactacttc	480	
240	aaaatcacta ctcaagaaat atg aag aat gtg gtg gct ttt gtt acg	533	
241	Met Lys Lys Met Asn Val Val Ala Phe Val Thr		
242	1 5 10		
244	ctg atc atc tct ttt ctt ctg ctt tct cag gtaaaactgtt aaaaccattt	583	
245	Leu Ile Ile Ser Phe Leu Leu Leu Ser Gln		
246	15 20		
248	tcaagactac cttttctcta tttcagacaa accaaagtaa aacaatgaaa aatctctctg	643	
250	gtcttcata g gta ctt gca gag ttg tca tcc agc aac aat gaa act	693	
251	Val Leu Ala Glu Leu Ser Ser Ser Asn Asn Glu Thr		

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252	25	30		
254	tcc tct gtt tct cag gtaagagtga	tacaaaaaca tactaaacaa	actttcaaga	748
255	Ser Ser Val Ser Gln			
256	35			
258	gagtaatata taaggaaatg ttggcttctt	tttttgttg ctaatcag	acg aat gac	805
259			Thr Asn Asp	
260		40		
262	gag aac caa act gcg gcg ttt aag aga aca tac cac cat cgt cca aga			853
263	Glu Asn Gln Thr Ala Ala Phe Lys Arg Thr Tyr His His Arg Pro Arg			
264	45	50	55	
266	atc agtagtcta ctcttcaac actctaattc	ctttgttcta agtattttt		906
267	Ile			
270	ttgcccccca caaccctttt tttattaaat gagccaattt	ttatagat tgt ggg cat		963
271			Cys Gly His	
272		60		
274	gca tgc gca agg aga tgc agt aag aca tcg agg aag aaa gtt tgt cac			1011
275	Ala Cys Ala Arg Arg Cys Ser Lys Thr Ser Arg Lys Lys Val Cys His			
276	65	70	75	
278	aga gcc tgt gga agt tgt tgt gcc aag tgt cag tgt gtg ccg ccg gga			1059
279	Arg Ala Cys Gly Ser Cys Ala Lys Cys Gln Cys Val Pro Pro Gly			
280	80	85	90	
282	acc tcc ggc aac aca gca tca tgt cct tgc tac gcc agt atc cgt aca			1107
283	Thr Ser Gly Asn Thr Ala Ser Cys Pro Cys Tyr Ala Ser Ile Arg Thr			
284	95	100	105	110
286	cat ggc aat aaa ctc aaa tgt cct taaaagactt	ctcatttctc aactatacg		1161
287	His Gly Asn Lys Leu Lys Cys Pro			
288	115			
290	tcatcttctg attatgttgc	ttctttgtt atgttgcattg	tgtgatgtgt gagcttatta	1221
292	ttatgttgcattt	tggtgacata attcaactat	ataatttgcata tcgattccga	1281
294	gagtgattttt	attggctattt	aagtttttt tttttttt tggttacaaa	1341
296	ttttaaacat	ctgattttat	aaacaacaaa gtttcatattt	1401
298	caaaatctcc	atacatatta	cacaacacaaa aaaatacaca	1461
300	ttcttgggttc	agagttgcata	tcttgcatttgc	1521
302	caaacacctt	ataaaagcttc	acgcgatcct tcaacgcattc	1581
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309	<212> TYPE: PRT			
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318	Leu Leu Leu Ser Gln Val Leu Ala Glu Leu Ser Ser Ser Ser Asn Asn			
319	20	25	30	
322	Glu Thr Ser Ser Val Ser Gln Thr Asn Asp Glu Asn Gln Thr Ala Ala			
323	35	40	45	
326	Phe Lys Arg Thr Tyr His His Arg Pro Arg Ile Cys Gly His Ala Cys			
327	50	55	60	
330	Ala Arg Arg Cys Ser Lys Thr Ser Arg Lys Lys Val Cys His Arg Ala			

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331	65	70	75	80												
334	Cys	Gly	Ser	Cys	Cys	Ala	Lys	Cys	Gln	Cys	Val	Pro	Pro	Gly	Thr	Ser
335				85				90							95	
338	Gly	Asn	Thr	Ala	Ser	Cys	Pro	Cys	Tyr	Ala	Ser	Ile	Arg	Thr	His	Gly
339				100				105							110	
342	Asn	Lys	Leu	Lys	Cys	Pro										
343				115												
346	<210>	SEQ	ID	NO:	5											
347	<211>	LENGTH:	1453													
348	<212>	TYPE:	DNA													
349	<213>	ORGANISM:	Arabidopsis	thaliana												
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353	<221>	NAME/KEY:	CDS													
354	<222>	LOCATION:	(501)..(533)													
355	<223>	OTHER INFORMATION:	signal peptide	(exon 1)												
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359	<222>	LOCATION:	(664)..(691)													
360	<223>	OTHER INFORMATION:	propeptide	(exon 2)												
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363	<221>	NAME/KEY:	CDS													
364	<222>	LOCATION:	(772)..(950)													
365	<223>	OTHER INFORMATION:	conserved cysteine motif	(exon 3)												
367	<400>	SEQUENCE:	5													
368	gaaaaaaaaa	agaaaaagata	atggccgta	ttaatatagt	tgaaaacttg	aaactacttt									60	
370	ttagtttga	tataatacag	tagacttaggg	atccagtta	gtttcttct	ttatttttag									120	
372	tttgtgttta	tgtttgattt	tacgtttta	tatgtaaata	agatattttta	cgaattatgg									180	
374	tttattttgg	gtagaagttg	tagaatgact	taaacaatca	agtggcagaa	tgagatatat									240	
376	aaagtaatat	aatatataat	cggttattaa	cttattgtac	atgtgaatga	ggaagcttac									300	
378	acacacacac	cttctataaa	tagctgacaa	aactgggtgt	tacacacaac	acattcataa									360	
380	atctctcaaa	gtaagaacta	agagctttac	tacagtccta	ctctctacac	atcttctctc									420	
382	tctctcaaga	gctagtcatg	gccaaactca	taacttcttt	tctcttactc	acaattttat									480	
384	tcactttcg	ttgtctcaact	atg tca	aaa gaa	gct gag	tac cat	cca gaa	agt							533	
385			Met Ser Lys Glu Ala	Glu Tyr His Pro	Glu Ser											
386		1	5	10												
388	gtaagttttt	attttttgg	aaaatagaaa	gtgttttttt	tataattcat	tcaatttttt									593	
390	ttgcctttcc	ctttcttattt	attgttataaa	atctaatacc	cgcgtttaaaa	tttttttttt									653	
392	aattaaacag	tat gga	cca gga	agt ctg	aaa tca	tac c	gtaagtaaaa								701	
393		Tyr	Gly	Pro	Gly	Ser	Leu	Lys	Ser	Tyr						
394		15	20													
396	acttcttctt	cttttatgaa	tcttgtttct	tattatataat	caaataaaaa	ctcgattttc									761	
398	atgattgcag	aa	tgt gga	caa tgc	aca agg	aga tgt	agc aac	aca							809	
399		Gln	Cys	Gly	Gly	Gln	Cys	Thr	Arg	Arg	Cys	Ser	Asn	Thr		
400		25	30													
402	aag tat	cat aag	cca tgc	atg ttc	ttc tgc	caa aag	tgt tgt	gct aaa							857	
403	Lys	Tyr	His	Lys	Pro	Cys	Met	Phe	Phe	Cys	Gln	Lys	Cys	Cys	Ala	Lys
404	35	40	45													
406	tgc	ctt	tgt	gtc	cct	cca	ggc	acg	tac	ggc	aac	aaa	caa	gtg	tgt	cct
407	Cys	Leu	Cys	Val	Pro	Pro	Gly	Thr	Tyr	Gly	Asn	Lys	Gln	Val	Cys	Pro

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Input Set : A:\PTO.AMC.txt
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:31; Xaa Pos. 2,4,7,8,9,10,11,12,13,14,16,17,18,20,21,24,25,27,31,34,36
Seq#:31; Xaa Pos. 37,38,39,41,44,45,46,47,48,49,50,52,53

Invalid Line Length:

The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:25; Line(s) 1786

VERIFICATION SUMMARY

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L:9 M:270 C: Current Application Number differs, Replaced Current Application No
L:9 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:517 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 7
L:1047 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 15
L:1311 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 19
L:2187 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:31 after pos.:0
M:341 Repeated in SeqNo=31